

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 09/884,901 A  
Source: JFW16  
Date Processed by STIC: 09/22/2005

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IFW16

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/884,901A

DATE: 09/22/2005

TIME: 09:55:14

Input Set : A:\UOFW17396seq.txt

Output Set: N:\CRF4\09222005\I884901A.raw

3 <110> APPLICANT: Miao, Carol  
 4 Kay, Mark  
 6 <120> TITLE OF INVENTION: Liver-Specific Gene Expression Cassettes, and Methods of Use  
 8 <130> FILE REFERENCE: UOFW-1-17396  
**C--> 10 <140> CURRENT APPLICATION NUMBER: US/09/884,901A**  
**C--> 10 <141> CURRENT FILING DATE: 2001-06-18**  
 10 <150> PRIOR APPLICATION NUMBER: US 60/212,902  
 11 <151> PRIOR FILING DATE: 2000-06-20  
 13 <160> NUMBER OF SEQ ID NOS: 18  
 15 <170> SOFTWARE: PatentIn version 3.0  
 17 <210> SEQ ID NO: 1  
 18 <211> LENGTH: 1438  
 19 <212> TYPE: DNA  
 20 <213> ORGANISM: HomoSapien  
 22 <400> SEQUENCE: 1  
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 25 atgctgtctt cttcaactaaa ttttgattac atgatttgac agcaatattg aagagtctaa 120  
 27 cagccagcac gcaggttggg aagtactggg tctttgttag cttaggtttc ttcttc 180  
 29 tttttaaaaac taaatagatc gacaatgctt atgatgcatt tatgtttaat aaacactgtt 240  
 31 cagttcatga tttggcatcg taattcctgt tagaaaaacat tcataccccc ggttaaaaaa 300  
 33 aattaaaaagt gggaaaaacaa agaaaatagca gaatatacg aaaaaaaaaa accacattat 360  
 35 tttgtttgg acttaccact ttgaaatcaa aatggaaac aaaaggcaca acaatggcct 420  
 37 tatttacaca aaaagtctga tttaagata tatgacattt caaggttca gaagtatgtt 480  
 39 atgaggtgtg tctctaattt tttaaattat atatctcaa tttaaagtt tagttaaaac 540  
 41 ataaaagatta acctttcatt agcaagctgt tagttatcac caaagcttt catgattag 600  
 43 gaaaaaatca ttttgtctct atgtcaaaca tcttgagtt gatatttgg gaaacacaat 660  
 45 actcagttga gttccctagg ggagaaaagg aagcttaaga attgacataa agagtaggaa 720  
 47 gttagctaatt gcaacatata tcactttgtt ttccacaac tacagtact ttatgtattt 780  
 49 cccagaggaa ggcatacagg gaagaaattha tcccatttgg acaaacacgca tgttctcaca 840  
 51 ggaagcattt atcacactta cttgtcaact ttctagaatc aatcttagta gctgacagta 900  
 53 ccaggatcag ggggtccaaac cctaagcacc cccagaaagg tgactggccc tgggttccc 960  
 55 actccagaca tggatgtcagg tggaaatcg acgtcgctgg accataatta ggcttctgtt 1020  
 57 cttcaggaga cattttttca aagtcatgg ggcaaccata ttctgaaaac agccagcca 1080  
 59 ggggtatggg tcactttgca aagatcctca atgagctatt ttcaagtgt gacaaagtgt 1140  
 61 gaagtttacc gtcatttgc gaaatttctt ttcatccaa agtaaattca aatatgatta 1200  
 63 gaaatctgac cttttattac tggaaattctc ttgactaaaa gtaaaattga attttatcc 1260  
 65 ctaaatctcc atgtgtatac agtactgtgg gaacatcaca gatattggct ccatgcccta 1320  
 67 aagagaaaatt ggcttcaga ttattttggat taaaaacaaa gactttctta agagatgtaa 1380  
 69 aattttcatg atgtttctt ttgtctaaa actaaagaat tatttttta catttcag 1438  
 72 <210> SEQ ID NO: 2  
 73 <211> LENGTH: 1413  
 74 <212> TYPE: DNA  
 75 <213> ORGANISM: HomoSapien

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77 <220> FEATURE:  
 78 <221> NAME/KEY: CDS  
 79 <222> LOCATION: (30)..(1412)  
 81 <400> SEQUENCE: 2

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83 Met Gln Arg Val Asn Met Ile Met	
84 1 5	
86 gca gaa tca cca ggc ctc atc acc atc tgc ctt tta gga tat cta ctc	101
87 Ala Glu Ser Pro Gly Leu Ile Thr Ile Cys Leu Leu Gly Tyr Leu Leu	
88 10 15 20	
90 agt gct gaa tgt aca gtt ttt ctt gat cat gaa aac gcc aac aaa att	149
91 Ser Ala Glu Cys Thr Val Phe Leu Asp His Glu Asn Ala Asn Lys Ile	
92 25 30 35 40	
94 ctg aat cgg cca aag agg tat aat tca ggt aaa ttg gaa gag ttt gtt	197
95 Leu Asn Arg Pro Lys Arg Tyr Asn Ser Gly Lys Leu Glu Glu Phe Val	
96 45 50 55	
98 caa ggg aac ctt gag aga gaa tgt atg gaa gaa aag tgt agt ttt gaa	245
99 Gln Gly Asn Leu Glu Arg Glu Cys Met Glu Glu Lys Cys Ser Phe Glu	
100 60 65 70	
102 gaa gca cga gaa gtt ttt gaa aac act gaa aga aca act gaa ttt tgg	293
103 Glu Ala Arg Glu Val Phe Glu Asn Thr Glu Arg Thr Thr Glu Phe Trp	
104 75 80 85	
106 aag cag tat gtt gat gga gat cag tgt gag tcc aat cca tgt tta aat	341
107 Lys Gln Tyr Val Asp Gly Asp Gln Cys Glu Ser Asn Pro Cys Leu Asn	
108 90 95 100	
110 ggc ggc agt tgc aag gat gac att aat tcc tat gaa tgt tgg tgt ccc	389
111 Gly Gly Ser Cys Lys Asp Asp Ile Asn Ser Tyr Glu Cys Trp Cys Pro	
112 105 110 115 120	
114 ttt gga ttt gaa gga aag aac tgt gaa tta gat gta aca tgt aac att	437
115 Phe Gly Phe Glu Gly Lys Asn Cys Glu Leu Asp Val Thr Cys Asn Ile	
116 125 130 135	
118 aag aat ggc aga tgc gag cag ttt tgt aaa aat agt gct gat aac aag	485
119 Lys Asn Gly Arg Cys Glu Gln Phe Cys Lys Asn Ser Ala Asp Asn Lys	
120 140 145 150	
122 gtg gtt tgc tcc tgt act gag gga tat cga ctt gca gaa aac cag aag	533
123 Val Val Cys Ser Cys Thr Glu Gly Tyr Arg Leu Ala Glu Asn Gln Lys	
124 155 160 165	
126 tcc tgt gaa cca gca gtg cca ttt cca tgt gga aga gtt tct gtt tca	581
127 Ser Cys Glu Pro Ala Val Pro Phe Pro Cys Gly Arg Val Ser Val Ser	
128 170 175 180	
130 caa act tct aag ctc acc cgt gct gag gct gtt ttt cct gat gtg gac	629
131 Gln Thr Ser Lys Leu Thr Arg Ala Glu Ala Val Phe Pro Asp Val Asp	
132 185 190 195 200	
134 tat gta aat tct act gaa gct gaa acc att ttg gat aac atc act caa	677
135 Tyr Val Asn Ser Thr Glu Ala Glu Thr Ile Leu Asp Asn Ile Thr Gln	
136 205 210 215	
138 agc acc caa tca ttt aat gac ttc act cgg gtt gtt ggt gga gaa gat	725
139 Ser Thr Gln Ser Phe Asn Asp Phe Thr Arg Val Val Gly Gly Glu Asp	
140 220 225 230	

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142	gcc	aaa	cca	ggc	caa	ttc	cct	tgg	cag	gtt	ttg	aat	ggc	aaa	gtt		773		
143	Ala	Lys	Pro	Gly	Gln	Phe	Pro	Trp	Gln	Val	Val	Leu	Asn	Gly	Lys	Val			
144			235					240				245							
146	gat	gca	ttc	tgt	gga	ggc	tct	atc	gtt	aat	gaa	aaa	tgg	att	gtc	act	821		
147	Asp	Ala	Phe	Cys	Gly	Gly	Ser	Ile	Val	Asn	Glu	Lys	Trp	Ile	Val	Thr			
148			250					255			260								
150	gct	gcc	cac	tgt	gtt	gaa	act	ggc	gtt	aaa	att	aca	gtt	gtc	gca	ggc	869		
151	Ala	Ala	His	Cys	Val	Glu	Thr	Gly	Val	Lys	Ile	Thr	Val	Val	Ala	Gly			
152			265				270			275		280							
154	gaa	cat	aat	att	gag	gag	aca	gaa	cat	aca	gag	caa	aag	cga	aat	gtg	917		
155	Glu	His	Asn	Ile	Glu	Glu	Thr	Glu	His	Thr	Glu	Gln	Lys	Arg	Asn	Val			
156			285				290			295									
158	att	cga	att	att	cct	cac	cac	aac	tac	aat	gca	gct	att	aat	aag	tac	965		
159	Ile	Arg	Ile	Ile	Pro	His	His	Asn	Tyr	Asn	Ala	Ala	Ile	Asn	Lys	Tyr			
160			300				305			310									
162	aac	cat	gac	att	gcc	ctt	ctg	gaa	ctg	gac	gaa	ccc	tta	gtg	cta	aac	1013		
163	Asn	His	Asp	Ile	Ala	Leu	Leu	Glu	Leu	Asp	Glu	Pro	Leu	Val	Leu	Asn			
164			315				320			325									
166	agc	tac	gtt	aca	cct	att	tgc	att	gct	gac	aag	gaa	tac	acg	aac	atc	1061		
167	Ser	Tyr	Val	Thr	Pro	Ile	Cys	Ile	Ala	Asp	Lys	Glu	Tyr	Thr	Asn	Ile			
168			330				335			340									
170	ttc	ctc	aaa	ttt	gga	tct	ggc	tat	gtt	agt	ggc	tgg	gga	aga	gtc	tcc	1109		
171	Phe	Leu	Lys	Phe	Gly	Ser	Gly	Tyr	Val	Ser	Gly	Trp	Gly	Arg	Val	Phe			
172			345				350			355		360							
174	cac	aaa	ggg	aga	tca	gct	tta	gtt	ctt	cag	tac	ctt	aga	gtt	cca	ctt	1157		
175	His	Lys	Gly	Arg	Ser	Ala	Leu	Val	Leu	Gln	Tyr	Leu	Arg	Val	Pro	Leu			
176			365				370			375									
178	gtt	gac	cga	aca	tgt	ctt	cga	tct	aca	aag	ttc	acc	atc	tat	aac		1205		
179	Val	Asp	Arg	Ala	Thr	Cys	Leu	Arg	Ser	Thr	Lys	Phe	Thr	Ile	Tyr	Asn			
180			380				385			390									
182	aac	atg	ttc	tgt	gct	ggc	ttc	cat	gaa	gga	ggc	ata	gtt	tca	tgt	caa	1253		
183	Asn	Met	Phe	Cys	Ala	Gly	Phe	His	Glu	Gly	Gly	Arg	Asp	Ser	Cys	Gln			
184			395				400			405									
186	gga	gat	agt	ggg	gga	ccc	cat	gtt	act	gaa	gtg	gaa	ggg	acc	agt	ttc	1301		
187	Gly	Asp	Ser	Gly	Gly	Pro	His	Val	Thr	Glu	Val	Glu	Gly	Thr	Ser	Phe			
188			410				415			420									
190	tta	act	gga	att	att	agc	tgg	ggc	gaa	gag	tgt	gca	atg	aaa	ggc	aaa	1349		
191	Leu	Thr	Gly	Ile	Ile	Ser	Trp	Gly	Glu	Glu	Cys	Ala	Met	Lys	Gly	Lys			
192			425				430			435		440							
194	tat	gga	ata	tat	acc	aag	gta	tcc	cgg	tat	gtc	aac	tgg	att	aag	gaa	1397		
195	Tyr	Gly	Ile	Tyr	Thr	Lys	Val	Ser	Arg	Tyr	Val	Asn	Trp	Ile	Lys	Glu			
196			445				450			455									
198	aaa	aca	aag	ctc	act	t										1413			
199	Lys	Thr	Lys	Leu	Thr														
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203	<210>	SEQ	ID	NO:	3														
204	<211>	LENGTH:	461																
205	<212>	TYPE:	PRT																
206	<213>	ORGANISM:	HomoSapien																

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208 <400> SEQUENCE: 3  
210 Met Gln Arg Val Asn Met Ile Met Ala Glu Ser Pro Gly Leu Ile Thr  
211 1 5 10 15  
214 Ile Cys Leu Leu Gly Tyr Leu Leu Ser Ala Glu Cys Thr Val Phe Leu  
215 20 25 30  
218 Asp His Glu Asn Ala Asn Lys Ile Leu Asn Arg Pro Lys Arg Tyr Asn  
219 35 40 45  
222 Ser Gly Lys Leu Glu Glu Phe Val Gln Gly Asn Leu Glu Arg Glu Cys  
223 50 55 60  
226 Met Glu Glu Lys Cys Ser Phe Glu Glu Ala Arg Glu Val Phe Glu Asn  
227 65 70 75 80  
230 Thr Glu Arg Thr Thr Glu Phe Trp Lys Gln Tyr Val Asp Gly Asp Gln  
231 85 90 95  
234 Cys Glu Ser Asn Pro Cys Leu Asn Gly Gly Ser Cys Lys Asp Asp Ile  
235 100 105 110  
238 Asn Ser Tyr Glu Cys Trp Cys Pro Phe Gly Phe Glu Gly Lys Asn Cys  
239 115 120 125  
242 Glu Leu Asp Val Thr Cys Asn Ile Lys Asn Gly Arg Cys Glu Gln Phe  
243 130 135 140  
246 Cys Lys Asn Ser Ala Asp Asn Lys Val Val Cys Ser Cys Thr Glu Gly  
247 145 150 155 160  
250 Tyr Arg Leu Ala Glu Asn Gln Lys Ser Cys Glu Pro Ala Val Pro Phe  
251 165 170 175  
254 Pro Cys Gly Arg Val Ser Val Ser Gln Thr Ser Lys Leu Thr Arg Ala  
255 180 185 190  
258 Glu Ala Val Phe Pro Asp Val Asp Tyr Val Asn Ser Thr Glu Ala Glu  
259 195 200 205  
262 Thr Ile Leu Asp Asn Ile Thr Gln Ser Thr Gln Ser Phe Asn Asp Phe  
263 210 215 220  
266 Thr Arg Val Val Gly Gly Glu Asp Ala Lys Pro Gly Gln Phe Pro Trp  
267 225 230 235 240  
270 Gln Val Val Leu Asn Gly Lys Val Asp Ala Phe Cys Gly Ser Ile  
271 245 250 255  
274 Val Asn Glu Lys Trp Ile Val Thr Ala Ala His Cys Val Glu Thr Gly  
275 260 265 270  
278 Val Lys Ile Thr Val Val Ala Gly Glu His Asn Ile Glu Glu Thr Glu  
279 275 280 285  
282 His Thr Glu Gln Lys Arg Asn Val Ile Arg Ile Ile Pro His His Asn  
283 290 295 300  
286 Tyr Asn Ala Ala Ile Asn Lys Tyr Asn His Asp Ile Ala Leu Leu Glu  
287 305 310 315 320  
290 Leu Asp Glu Pro Leu Val Leu Asn Ser Tyr Val Thr Pro Ile Cys Ile  
291 325 330 335  
294 Ala Asp Lys Glu Tyr Thr Asn Ile Phe Leu Lys Phe Gly Ser Gly Tyr  
295 340 345 350  
298 Val Ser Gly Trp Gly Arg Val Phe His Lys Gly Arg Ser Ala Leu Val  
299 355 360 365  
302 Leu Gln Tyr Leu Arg Val Pro Leu Val Asp Arg Ala Thr Cys Leu Arg  
303 370 375 380

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306 Ser Thr Lys Phe Thr Ile Tyr Asn Asn Met Phe Cys Ala Gly Phe His  
 307 385 390 395 400  
 310 Glu Gly Gly Arg Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro His Val  
 311 405 410 415  
 314 Thr Glu Val Glu Gly Thr Ser Phe Leu Thr Gly Ile Ile Ser Trp Gly  
 315 420 425 430  
 318 Glu Glu Cys Ala Met Lys Gly Lys Tyr Gly Ile Tyr Thr Lys Val Ser  
 319 435 440 445  
 322 Arg Tyr Val Asn Trp Ile Lys Glu Lys Thr Lys Leu Thr  
 323 450 455 460

326 &lt;210&gt; SEQ ID NO: 4

327 &lt;211&gt; LENGTH: 771

328 &lt;212&gt; TYPE: DNA

329 &lt;213&gt; ORGANISM: HomoSapien

331 &lt;400&gt; SEQUENCE: 4

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 334 cccatcctcc agcagctgtt tgtgtgctgc ctctgaagtc cacactgaac aaacttcagc 120  
 336 ctactcatgt ccctaaaatg ggcaaacatt gcaagcagca aacagcaaac acacagccct 180  
 338 ccctgcctgc tgaccttgga gctggggcag aggtcagaga cctctctggg cccatgccac 240  
 340 ctccaacatc cactcgaccc cttggaattt cggtggagag gagcagaggt tgcctggcg 300  
 342 tggttaggt agtgtgagag gtcgggggtt caaaaccact tgctgggtgg ggagtgcgtca 360  
 344 gtaagtggct atgccccgac cccgaagctt gttttccat ctgtacaatg gaaatgataa 420  
 346 agacgcccattt ctgatagggtt ttttgtggca aataaacatt tggtttttt gttttgtttt 480  
 348 gttttgtttt ttgagatgga gtttgctct gtcggccagg ctggagtgcgtca gtgacacaat 540  
 350 ctcatctcac cacaaccttc ccctgcctca gcctcccaag tagctggat tacaaggcatg 600  
 352 tgccaccaca cctggtaat tttctatttt tagtagagac gggtttctcc atgttggtca 660  
 354 gcctcagcct cccaaatggaa tgggattaca ggcctgtgcc accacacccg gctaattttt 720  
 356 tcatttttg acagggacgg gtttccatca tggtggcgtt gctcctcttag a 771

359 &lt;210&gt; SEQ ID NO: 5

360 &lt;211&gt; LENGTH: 418

361 &lt;212&gt; TYPE: DNA

362 &lt;213&gt; ORGANISM: HomoSapien

364 &lt;400&gt; SEQUENCE: 5

365 ggatcttgc accagtggaa cagccactaa ggattctgca gtgagagcag agggccagct 60  
 367 aagtggact ctcccagaga ctgtctgact caccccaccc cctccaccc ggacacagga 120  
 369 cgctgtgggt tctgagccag gtacaatgac tccttcgggt aagtgcagtg gaagctgtac 180  
 371 actgcccagg caaagcgtcc gggcagcgtt ggcggccac tcagatccca gccagtggac 240  
 373 ttagccccctg tttgccttc cgataactgg ggtgacctt gttaatattt accaggcc 300  
 375 tccccctggc cccctctggc tccactgctt aaatacggac gaggacaggg ccctgtctcc 360  
 377 tcagcttcag gcaccaccac tgacctgggaa cagtgaatga tccccctgtat ctggggcc 418

380 &lt;210&gt; SEQ ID NO: 6

381 &lt;211&gt; LENGTH: 282

382 &lt;212&gt; TYPE: DNA

383 &lt;213&gt; ORGANISM: Bos taurus

385 &lt;400&gt; SEQUENCE: 6

386 cccgggggat cagcctcgac tgccttctt agttgccagc catctgttgt ttgccccctcc 60  
 388 cccgtgcctt ccttgaccctt ggaagggtgcc actcccactg tccttccta ataaaaatgg 120  
 390 gaaattgcat cgcatgtctt gatgttgtt cattctattt tgggggggtgg ggtggggcag 180  
 392 gacagcaagg gggaggattt ggaagacaat agcaggcatg ctggggatgc ggtgggtct 240

**VERIFICATION SUMMARY**

PATENT APPLICATION: US/09/884,901A

DATE: 09/22/2005

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Input Set : A:\UOFW17396seq.txt

Output Set: N:\CRF4\09222005\I884901A.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date